

SEQUENCE LISTING

<110> BANYU PHARMACEUTICAL CO., LTD.

<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP) BINDING PROTEIN-COUPLED RECEPTOR
PROTEINS

<130> B1-103PCT

<140>

<141>

<150> PCT/JP98/05967

<151> 1998-12-25

<150> JP 1999-145661

<151> 1999-05-25

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 413

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

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Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100 105 110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225

230

235

240

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245

250

255

T0330:050T0330

260 265 270

275 280 285

290 295 300

305 310 315 320

325 330 335

340 345 350

355 360 365

370 375 380

385 390 395 400

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

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<210> 2

<211> 1239

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(1239)

<400> 2

atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tgc ggc act ctg 48

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1 5 10 15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tgc gct gcc 96

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 144

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

TTGGGAGCGCGCCGACGGGCTGATGAACGCGTCGGCCTCTG

50 55 60

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg 480

cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc 768
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
245 250 255

agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg 816

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260

265

270

cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc 864

His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

275

280

285

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc 912

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

290

295

300

atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tgc cgg 960

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

305

310

315

320

gac aag aag gtg gcc aag tgc ctg gcc atc atc gtg agc atc ttt ggg 1008

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

325

330

335

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc 1056

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

340

345

350

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1104

F03390-2507650

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

355

360

365

ctg tgg gcc aac tgc gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1152

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

370

375

380

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1200

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

385

390

395

400

aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag 1239

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

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<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 3

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<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 4

ccataaaagn nggggttgac

20

<210> 5

<211> 2700

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (351)..(1589)

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accgacgcac cgcgggcggc iggagctcgg ctttgccttc gctgcagcag ccgcgccgcc 120

cgccccactc cgcicagatt ccgacaccag cccctctgg atcgccctcc tggactctag 180

cccgggctct tgciccgacc ccgcggacca tgcicgggc gccccccgga aaaccgggct 240

ggcggaagag ccggcaaaga ttaggctcac gagcgggggc cccacccggc caccagctc 300

tccgcccgtg ccttgcggg tgtcccgag ccgigtgagc ctgctgggcc atg gag 356

Met Glu

1

cgc gcg ccg ccc gac ggg ctg atg aac gcg tgc ggc act ctg gcc gga 404

Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly

5

10

15

gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tgc gct gcc tgg acc 452

Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr

20

25

30

gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg 500

Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu

35

40

45

50

ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tgc agc ctc cgc 548

Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg

55

60

65

11/47

Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu

80

Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly

95

Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp

110

Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr

130

Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln

145

Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu

160

gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct 884

Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser

165

170

175

ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac 932

Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr

180

185

190

aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc 980

Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro

195

200

205

210

ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac atc cag 1028

Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln

215

220

225

agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa 1076

Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu

230

235

240

ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc agc tgc 1124

Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro Ser Cys

245

250

255

igg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg cac agc 1172

Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu His Ser

260

265

270

T0300:00000000

gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac tac agc 1508

Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser

375

380

385

ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc aag gtc 1556

Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val

390

395

400

cag ccc cac ggc tcc ctg gag cag tgc tgg aag tgagcagctg cccaccctt 1609

Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

405

410

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ccatgtctcg ctccaaatgc catggcggcc tcttagatca tcaaccccg c agtggggtag 1729

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gccacattct ccttcaccac acagaagaga caatccagga gtcccaggca tgccttccac 1849

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cgcacacaca ctgcaaac ctcctctctc ccagaagagc tggggacgat gcccttgtct 2089

1556-1609-1669-1729-1789-1849-1909-1969-2029-2089

gccactgtct ctgtcttaat cccagagcct ggctccttat cccccactct ccttcaact 2149

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aaaaaaaaa a 2700

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 6

cgaggatccg tgaggctccg gggcccg

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<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 7

cgggtaagct tcacgacacc tgaaatggaa ga

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<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 8

ccctctgcat cccattgtac gtacc

24

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 9

cttccgccgg gccctcacca a

21

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 10

acagacacgg cggggctcac

20

<210> 11

<211> 1350

<212> DNA

<213> Homo sapiens

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<221> exon

<222> (280)..(557)

<400> 11

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ccccctggca ccgcctgctc tggccccggc cccggccccg cggaccaatgc gctgggcgcc 180

cccaggggaa cccgacccgg ccaagggcc gcaaagacga ggctcccggg ccggggcccc 240

tcccgccgc ccagctctcg gccggcgccc tgcccccggt cccggagccg cgtgagcctg 300

TTGGGCTCAC

caggctctgc tgccggctgg ggggcggggc acgcggaggg ggctggagcg ccagacacct 1080

gttggggctg tgaggtagct ctcccagacg ctccaagccc gcttggcagt agtagtagcg 1140

gctggcggct ggaggctgca accaagtgcc ctctcagcca ggagaaagge ttctccttg 1200

tctaagctga gaccgagggc tgccagcgc cagggtaggg gctggagtc agcgggggag 1260

gggagaagga aatigtcttc ttctctctt tgagggtgg gagggctgga cagaagtcga 1320

gggaatcccg actccaggct ctgggggtc 1350

<210> 12

<211> 448

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (259)..(425)

<400> 12

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gggagctatg tgggggtgaa ggctggcggc agggcagagt ttgiggciga caccaggtg 120

TGAGGCTGCTCTCCAGACGCTCCAAGCCC

•

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U

0

0

8

<213> Homo sapiens

 $\langle 222 \rangle \quad (293) \dots (1209)$

gagctcacag ctggtagggg gtggtaaaca ggcagcctag cagagagiga gggttcaggt 60

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agtggggagg gtagaggaa gggaggggaa agagggaggg agggaggaca ggaggggaaa 180

ggaggagcat tgcctgag ggaagggccc acataggggc ccacaggcta cgggggagca 240

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catccccgag ggccactgct atcccgagtt ctctacaac tggctacttc tcatcacggc 480

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..

ggccaactcg gctgtcaacc ctgtcctcta cctctgtgc caccacagct tccgccgggc 1140

cttcaccaag ctgctctgcc ccagaagct caaaatccag cccacagct cctggagca 1200

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tcttgggcat ctggccctgc tgcctctac ccggctcgtt ccccagggg tgagccccgc 1320

cgctctgtg gccctctctt aatgccacgg cagccacct gccatggagg cgcttccctg 1380

ggttggccag agggccctc actggctgga ctggaggctg ggtggccggc cctgcccccc 1440

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acattctggc tccaccggga gggacagctt ggaggicca gacatgctgc ccacccctg 1500

ctgtgcccc ccttcgcag ttacttggtt gtgttcttc caaagcaag acctgggtgt 1560

gtccaggct tctgccccta gcagtttgc tctgcacgtg cacacacctg cacacccctg 1620

cacacacctg cacaccgtc ctctccccg acaagcccag gacactgctt ttgtgcctt 1680

ctgtctcttg cataagcctc aggcctggcc ctctacccc tcttcccacc aacictctct 1740

gcccccaaaa gtgtcaaggg gccctaggaa cctcgaagct gtctcttgct tttccattct 1800

gggtgttttc agaaagatga agaagaaaac atgictgtga acttgatgtt cctgggaigt 1860

ttaatcaaga gagacaaaat tgctgaggag ctc 1893

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 14

tgaacgcttc gggggcgctg 20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

TOSSO ESTERO

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 15

gagatggcga ggttgagcag g

21

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 16

ggctccaagc catcggcgtc

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<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially

Sequence = 5'-GGCTCCAAGC CATCGGCCTC-3'

synthesized primer sequence

<400> 17

ctcacttcca gcagtgtcc

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<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 18

gcctccgcac ccagaacaac

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<210> 19

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

TO3390-250T6460

<400> 19

tgcgcctctg gatgttcag

19

<210> 20

<211> 453

<212> PRT

<213> Homo sapiens

<400> 20

Met Glu Arg Ala Pro Pro Asp Gly Pro Leu Asn Ala Ser Gly Ala Leu

1

5

10

15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20

25

30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35

40

45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50

55

60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65

70

75

80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85

90

95

T05590:EST6600

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala

355 360 365

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys

435

440

445

Lys Lys Thr Cys Leu

450

<210> 21

<211> 2050

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (271)..(1629)

<400> 21

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aggctgcgga ggcagagctg catgctgggt gcgggaagag gtgggctccg tcgcggagtc 180

gctgagtcgc tgccctittt gitagtcttg cagtctagta tggccccat ttgcccttcc 240

actcccgag ccgcgtgagc ctgcggggcc atg gag cgc gcg ccg ccc gac ggg 294

Met Glu Arg Ala Pro Pro Asp Gly

1

5

ccg ctg aac gct tcg ggg gcg ctg gcg ggc gag gcg gcg gcg gcg ggc 342

Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly

10

15

20

ggg gcg cgc ggc ttc tcg gca gcc tgg acc gcg gtg ctg gcc gcg ctc 390

Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu

25

30

35

40

atg gcg ctg ctc atc gtg gcc acg gtg ctg ggc aac gcg ctg gtc atg 438

Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met

45

50

55

T0330-030T030

60 65 70

75 80 - 85

90 95 100

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 Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val
 125 130 135

gtg cgg aag atg ctg ctg gtg tgg gig ctg gcc ttc ctg ctg tac gga 774
Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly

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cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc 822			
Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro			
170	175	180	
gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc 870			
Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile			
185	190	195	200
acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc 918			
Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe			
	205	210	215
ttt aac ctc agc atc tac ctg aac atc cag agg cgc acc cgc ctc cgg 966			
Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg			
	220	225	230
ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc 1014			
Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Pro Glu Ala			
235	240	245	
cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag 1062			
Gln Pro Ser Pro Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys			
250	255	260	

gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg 1398
Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu

365

370

375

cig atg atc atc cgg gcc gcc tgc cat ggc cac tgc gtc cct gac tac 1446

Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr

380

385

390

tgg tac gaa acc tcc ttc tgg ctc cig tgg gcc aac tgc gct gtc aac 1494

Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn

395

400

405

cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc 1542

Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr

410

415

420

aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg 1590

Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu

425

430

435

440

gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat 1639

Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu

445

450

gttccctggga tgttttaatca agagagacaa aatigctgag gagctcaggg ctggatiggc 1699

agggtgtgggc tcccacgccc tcttccctcc gctaaggett ccggctgagc tgtgccagct 1759

T0350-030T0350

•

1

Or

1.

1

3

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

atcattagga gcgtgtangg

<210> 24

<211> 20

<212> DNA

⟨213⟩ Artificial Sequence

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

tgctctggga caccaatcttc

20

$\langle 210 \rangle$ 25

$\langle 211 \rangle$ 445

<212> PRT

<213> Rattus norvegicus

<400> 25

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1

5

10

15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20

25

30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35

40

45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50

55

60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65

70

75

80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85

90

95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

T0330-0304

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225

230

235

240

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245

250

255

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260

265

270

T03330 = GATC0000

His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu

275

280

285

Ala Ala Leu Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Ser Pro Thr

290

295

300

Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

305

310

315

320

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

325

330

335

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

340

345

350

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

355

360

365

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

T0530-250700

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

435

440

445

<210> 26

<211> 1953

<212> DNA

<213> Rattus norvegicus

<220>

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<400> 26

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ctggactcta gcccgggctc ttgctccgac cccgcggacc atgctccggg cgccccccgg 180

aaaaccgggc tgggcgaaga gccggcaaag attaggctca cgagcggggg ccccaccggg 240

•

1

1

1

1

1

1

1

0

110

125

140

160

175

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195	200	205	
-			
acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac	973		
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn			
210	215	220	
atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc	1021		
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly			
225	230	235	240
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc	1069		
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro			
245	250	255	
agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg	1117		
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu			
260	265	270	
cac agg tat ggg gtg ggt gag gca ggc cct ggt gtt gag gct ggg gag	1165		
His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu			
275	280	285	
gct gcc ctc ggg ggt ggc agt ggt gga ggt gct gct gcc tcg ccc acc	1213		
Ala Ala Leu Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Ser Pro Thr			
290	295	300	

ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1549
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1597

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag tgagcagctg 1646

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

435

440

445

ccccacccctt ctgaggccag gcccttgtac ttgtttgagt gggcagccgg agcgtgggcg 1706

gggcccttggt ccatgtctcg ctccaaatgc catggcggcc tcttagatca tcaaccccg 1766

agtggggtag catggcaggt gggccaagag ccctagittg tggagctaga gtgtgctggt 1826

tagctctgcc gcacattctc ctccaccaca cagaagagac aatccaggag tcccaggcat 1886

gccttcacct acacacacac acacacacac acacacacac acaccacagt gcagtgccag 1946

tgaigtc

1953

1597 1646 1706 1766 1826 1886 1946 1953